



SEQUENCE LISTING

<110> AMRAD Operations Pty Ltd

<120> A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
FAMILY OF APOPTOSIS-CONTROLLING GENES

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<140> 09/925,674

<141> 2001-08-09

<150> PN8965

<151> 1996-03-27

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<170> PatentIn Ver. 2.1

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33

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 Phe Val Gly Tyr Lys Leu Arg Gln Lys Gly Tyr Val Cys Gly Ala Gly
 20 25 30

ccc ggg gag ggc cca gca gct gac ccg ctg cac caa gcc atg cgg gca 144
 Pro Gly Glu Gly Pro Ala Ala Asp Pro Leu His Gln Ala Met Arg Ala
 35 40 45

gct gga gat gag ttc gag acc cgc ttc cgg cgc acc ttc tct gat ctg 192
 Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
 50 55 60

gcg gct cag ctg cat gtg acc cca ggc tca gcc cag caa cgc ttc acc 240
 Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
 65 70 75 80

cag gtc tcc gac gaa ctt ttt caa ggg ggc ccc aac tgg ggc cgc ctt 288
 Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
 85 90 95

gta gcc ttc ttt ctg ttt ggg gct gca ctg tgt gct gag agt gtc aac 336
 Val Ala Phe Phe Leu Phe Gly Ala Leu Cys Ala Glu Ser Val Asn
 100 105 110

aag gag atg gaa cca ctg gtg gga caa gtg cag gag tgg atg gtg gcc 384
 Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
 115 120 125

tac ctg gag acg cgg ctg gtc gac tgg atc cac agc agt ggg ggc tgg 432
 Tyr Leu Glu Thr Arg Leu Val Asp Trp Ile His Ser Ser Gly Gly Trp
 130 135 140

gcg gag ttc aca gct cta tac ggg gac ggg gcc ctg gag gag gcg cgg 480
 Ala Glu Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Glu Ala Arg
 145 150 155 160

cgt ctg cgg gag ggg aac tgg gca tca gtg agg aca gtg ctg acg ggg 528
 Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
 165 170 175

gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc 576
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      35           40          45

Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu
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Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr
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Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu
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Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn
      100          105          110

Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Glu Trp Met Val Ala
      115          120          125

Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp
      130          135          140

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Arg Leu Arg Glu Gly Asn Trp Ala Ser Val Arg Thr Val Leu Thr Gly
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Ala Val Ala Leu Gly Ala Leu Val Thr Val Gly Ala Phe Phe Ala Ser
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Lys
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Ala Gly Asp Glu Phe Glu Thr Arg Phe Arg Arg Thr Phe Ser Asp Leu	
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gcc gct cag cta cac gtg acc cca ggc tca gcc cag caa cgc ttc acc	240
Ala Ala Gln Leu His Val Thr Pro Gly Ser Ala Gln Gln Arg Phe Thr	
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cag gtt tcc gac gaa ctt ttc caa ggg ggc cct aac tgg ggc cgt ctt	288
Gln Val Ser Asp Glu Leu Phe Gln Gly Gly Pro Asn Trp Gly Arg Leu	
85 90 95	
gtg gca ttc ttt gtc ttt ggg gct gcc ctg tgt gct gag agt gtc aac	336
Val Ala Phe Phe Val Phe Gly Ala Ala Leu Cys Ala Glu Ser Val Asn	
100 105 110	
aaa gaa atg gag cct ttg gtg gga caa gtc cag gat tgg atc gtg gcc	384
Lys Glu Met Glu Pro Leu Val Gly Gln Val Gln Asp Trp Ile Val Ala	
115 120 125	
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Tyr Leu Glu Thr Arg Leu Ala Asp Trp Ile His Ser Ser Gly Gly Trp	
130 135 140	
gcg gac ttc aca gct cta tac ggg gac ggg gcc ctg gag gac gca cgg	480
Ala Asp Phe Thr Ala Leu Tyr Gly Asp Gly Ala Leu Glu Asp Ala Arg	
145 150 155 160	
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Arg Leu Arg Glu Gly Asn Trp Ala Val Ser Thr Val Val Thr Gly Ala	
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gcc gtg gca ctg ggg gcc ctg gta act gta ggg gcc ttt ttt gct agc	576
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Lys	Glu	Met	Glu	Pro	Leu	Val	Gly	Gln	Val	Gln	Asp	Trp	Met	Val	Ala		
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Ala	Val	Ala	Leu	Gly	Ala	Leu	Val	Thr	Val	Gly	Ala	Phe	Phe	Ala	Ser		
			180					185					190				
Lys																	